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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/848,967	05/04/2001	Emanuel Calenoff	21417/92378	6936
23644	7590	01/10/2006	EXAMINER	
BARNES & THORNBURG, LLP			CHEU, CHANGHWA J	
P.O. BOX 2786			ART UNIT	
CHICAGO, IL 60690-2786			PAPER NUMBER	

1641

DATE MAILED: 01/10/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/848,967	CALENOFF ET AL.	
	Examiner	Art Unit	
	Jacob Cheu	1641	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 07 October 2005.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-3,17-19,21 and 22 is/are pending in the application.
- 4a) Of the above claim(s) 4-16 and 20 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-3,17-19,21 and 22 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|---|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413) |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. _____ |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| Paper No(s)/Mail Date _____ | 6) <input type="checkbox"/> Other: _____ |

DETAILED ACTION

Applicant's amendment filed on 10/7/2005 has been received and entered into record and considered.

Claims 1-3, 17-19 and 21-22 are under examination. Claims 4-16 and 20 are withdrawn from further consideration.

Claim Rejections - 35 USC § 112

1. The following is a quotation of the second paragraph of 35 U.S.C. 112:
The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-3, 17-19, 21 & 22 are rejected under 35 USC §112, second paragraph as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

With respect to claim 1, line 3, a target disease or “condition” is vague and indefinite. It is not clear what is this “condition”. There is no definition of this “condition” in the specification. It is not clear whether this condition (line 3) is the same as the “condition specific immune response in a host”. Similarly, step (f) also suffers the same problem.

With respect to claim 1, step (d), “net sequence homology” is vague and confusing. It is not clear what constitutes “net sequence homology”. There is no definition in the specification. Furthermore, “net sequence homology” is not used by one ordinary skill in the art. Examiner has searched such terminology in the US, European and Japanese patent applications and issued patents. However, only applicant uses such term. Applicant needs to provide clear definition with respect to the definition of this term, particularly from specification.

With respect to claim 1, step (e), “overall homology” is vague and definition. Similarly, this term is also without clear definition from the specification.

Comparative protein

Step (d) of amended claim 1 requires that the peptides of the claim have “an amino acid net sequence homology of 50 percent or less as compared with contiguous amino acid sequences of a comparative protein defined by a matching algorithm.”

Fundamental to an understanding of the claim is what is meant by “comparative protein.” The specification contains at least two definitions of “comparative proteins.” In paragraph [008] occurs a definition:

(c) a net amino acid sequence homology of less than 50 percent as compared to the structure of peptide regions on proteins of related non-target proteins (the “comparative” proteins);

whereas paragraph [067] states

Computer-aided searches are performed to locate at least two amino acid sequences that show no more than 50% homology with the target protein. These sequences are designated non-targeted, non-specific or comparative proteins.

It is noted that the definition in paragraph [067] is followed by an example of two related polypeptides.

In the response of February 18, 2004 applicant stated:

However, “**comparative proteins**” are extensively defined in the specification e.g., on page 2, lines 35-36 to page 3, lines 1-7, and page 12, lines 29-31, the specification describes “comparative proteins” as non-targeted and non-specific proteins that show no more than 50% homology with the targeted protein as determined by computer-aided analysis.

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The examiner does not find the cited passages provide an extensive definition whatsoever especially when read in conjunction with applicant's remarks.

The definitions at [008] and [067] are not the same. The definition of [008] requires that the sequence of a peptide share less than 50% homology to the sequence in the polypeptide to which it is aligned whereas [067] requires that the sequence of the polypeptides from which the peptide sequence arises share less than 50% homology.

The response of July 16, 2004 was accompanied by an Expert Declaration and addressed in part the issue of "comparative proteins." Dr. Anderson states in paragraph 4. b.

. . . Then follows the unique and inventive steps of Calenoff-Ditlow: The protein surface probable sequences (the PSP sequences) are compared to all other known proteins (comparative proteins) for possible sequence homologies and those which are less than 50% homologous to sequences of other proteins, and which have less than 4 or more contiguous amino acids identical to the comparative protein sequences, are selected for use as immunogens and are the peptides for which composition claims are made.

In the response of April 25, 2005 applicant states

A peptide satisfying 1 (a), (b) and (c) is then tested against other peptides of the same length, that is, from "comparative proteins", **not** from the target protein. This is to eliminate peptides that cross react with the non-target proteins.

The response also includes a table designated **Comparative Proteins** at page 10 which more extensively defines comparative proteins. Note particularly the citation to page 3, lines 23-26 of the specification which state:

[0010] Non-target proteins are selected for comparative purposes, by scanning for all available sequence matches in computer data banks. Amino acid sequences of at least 4 in length are selected from at least 1 of the protein sequences that showed some degree of homology to the target protein. Closest matches are preferred.

and to page 5, lines 5-34

[0012] To reiterate, for the methods of the present invention, a disease or condition is targeted, for which an organism, agent or tissue is identified that is known to be causative of, or associated with, the targeted disease or condition for which diagnosis and/or treatment is sought. Proteins from the organism, agent or tissue are selected from databases, e.g. the NIH gene bank, which is available on the internet. These proteins are called "target" proteins. Functionally specific peptide antigen candidates are identified from within the amino acid structure of each protein on the basis of being hydrophilic and therefore likely to be on the outer surface of the protein. The amino acid structure of the candidate peptides are then compared to the amino acid structures found in individual non-target, (non-specific), proteins by using computer matching programs such as BLAST. Functionally specific peptide antigens are selected on the basis of having no more than 50% amino acid matching (sequence homology) with the comparative protein peptide sequences. Furthermore, whatever candidate antigen sequences satisfy this criteria must also possess no more than three contiguous (immediately adjacent to one another) amino acids which are sequentially homologous to amino acids matching foreign protein amino acid sequences.

and to page 6, lines 7-10

[0016] (c) a net sequence homology of 50 percent or less as compared to the structure of single non-specific proteins, that is proteins from non-target microorganisms, or proteins from non-target tissues.

In the final three portions of the Table applicant provides an example purportedly in keeping with the definition of comparative protein as set forth earlier in the table. These portions relate to the comparison of *H. pylori* sequences to two related sequences.

All of the foregoing creates a paradox as to what a "comparative protein" is and how one goes about choosing comparative proteins so as to practice the invention.

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If one accepts the definition set forth by applicant's declarant then candidate peptides which meet steps 1(a)-(c) would be screened using a program such as BLAST and only those which showed less than 50% homology to contiguous sequences in the data base would be selected for further testing as set forth in steps (e) and (f).

In disputing a prior art rejection applicant (Response of October 7, 2005) stated that the peptides of Malorny did not satisfy the claims because the peptide sequences were found in a plurality of polypeptides (see pages 8-9 of the response). This line of argument is consistent with the interpretation set forth by applicant's declarant.

However, applicant's specification clearly and convincingly contradicts the foregoing. SEQ ID NO: 14 is indicated in Figure 6 as representing a peptide within the scope of the claims as is SEQ ID NO: 21. Therefore, these sequences must necessarily meet the requirements of steps (d)-(f). Attached is a partial comparison run on NCBI BLAST which clearly shows that neither cited sequence meets the criteria of steps (d)-(f) (See BLAST search A1 and A2).

Furthermore, take SEQ ID No. 3 fragment (KNLESYQKDA) as an example. Applicant used the computer aided screening method as disclosed in the specification to identify this fragment satisfying all the criteria as recited in claim 1 (a) to (f). However, a contiguous portion, i.e. YQKDA (more than 3), has been found out homology to many proteins (See BLAST (B) compared with BLAS (C)). The BLAST search results show the discrepancy and contradiction with respect to step (d)-(e) of claim 1.

One is now left to search the specification for a definition of "comparative proteins" which will permit one to obtain peptides which meet the criteria of steps (d)-(f) of claim 1. No such definition is present in the specification or claims as originally filed.

Consider paragraph [067] in relation to a definition of "comparative proteins." There is absolutely no explanation as to why the two sequences presented were chosen from the

many available sequences in the NCBI database nor why only two were selected for purposes of comparison.

Enablement Rejection

2. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-3, 17-19, 21 & 22 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

Factors to be considered in determining whether a disclosure would require undue experimentation have been summarized by the board in *Ex parte Forman*. They include (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims. (*In re Wands*, 8 USPQ2d 1400-1408 (Fed.Cir. 1988), *Ex parte Forman*, 230 USPQ 546-549 (BdPtApp&Int 1986))

With respect to (1) the quantity of experimentation necessary no accurate evaluation can be made since it is not apparent if the requirements set forth in steps (d)-(f) of claim 1 can be met.

In support of this position it is noted that SEQ ID NO:s 14 and 21 which are asserted to be within the scope of the claims clearly fail step (d) of claim 1.

Step (e) requires that peptides within the scope of the claim share three or fewer contiguous amino acids "of the part of the comparative protein matched for over all homology." The exact meaning of this phrase is not set forth in the specification, however, if one accepts the Anderson declaration it would appear to mean that candidate peptides would not share three contiguous amino acids with any polypeptide sequence in the NCBI database.

Nor can one reasonably conclude that this step reasonably leads to the requisite epitopes given Figure 3 of Geysen et al. (J Mol. Recognition Vol. 1, page 32, 1988). Figure 3 suggests that three contiguous amino acids are often critical to reactivity which permits the inference that one might select candidate antigens which do not share three contiguous so as to avoid cross reactivity, however, there is nothing which indicates that such a selection actually results in selecting candidate peptides which would not show cross reactivity.

Step (f) appears to require screening of candidate peptides against infected and control populations. The actual assays for such screening may be enabled, however, the diseases and candidate peptides which would satisfy such assays are not readily apparent because one of skill in the art cannot a priori predict which disease antigen has a reasonable probability of containing linear epitopes recognized by patient antibodies or contains T-cell epitopes.

With respect to (2), claim 1 has guidance to the extent that the steps are definite and one could attempt to follow them.

With respect to (3) there are no working examples which meet claim 1 as currently amended.

With respect to (4) the invention would appear to be directed toward obtaining unique epitopes present on antigens so that one could reliably detect the presence of said antigen with minimal expectation of false positives arising from cross reactive epitopes. Whether such a goal can be achieved is in question in view of Geysen et al. (1988) which sets forth that the probability that a polyclonal antisera will contain antibodies directed against a randomly chosen antigen as about 1 in 40.

With respect to (5) the prior art is rife with epitope predicting algorithms which have shown various degrees of efficacy.

With respect to (6) the level of skill in the art in designing algorithms and developing immunoassays is high.

With respect to (7) there are currently no algorithms in the prior art which predict unique epitopes.

With respect to (8) the claims currently embrace mixtures of peptides for any possible antigen.

Response to Applicant's Arguments

3. Applicant's arguments with respect to claims 1-3, 17-19 and 21-22 have been considered but are moot in view of the new ground(s) of rejection.

4. Accordingly, the finality rejections of 35 USC 102 by reference of Rose et al. (WO 97/12042), Malorny et al. (J. Bacteriology 1998, Vol. 180: 1323) and Geysen et al. (US 5595915) are withdrawn.

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Conclusion

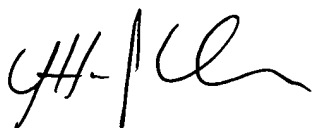
5. No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jacob Cheu whose telephone number is 571-272-0814. The examiner can normally be reached on 9:00-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Long Le can be reached on 571-272-0823. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Jacob Cheu
Examiner



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December 30 2005



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